CDC7 Gene Structure

FIGURE 1

CDC27A1 Gene Structure
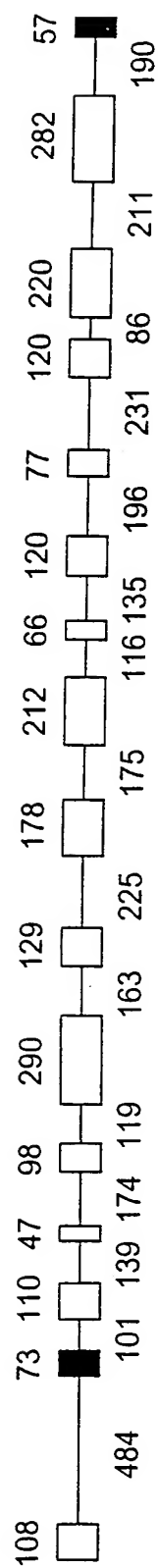
57 190 282 211 120 220 86 77 231 120 196 66 116 135 212 175 178 225 129 163 290 119 98 174 47 139 110 101 73 484 108

FIGURE 2

Fig. 3

```
                            ATGTCAGAAAACTCGGAACCGCGTCAACTCGAGAATTCTACA
  1  ---------+---------+---------+---------+---------+---------+  60
     TCTAAGTGTCGTAAACGTTACAGTCTTTTGAGCCTTGGCGCAGTTGAGCTCTTAAGATGT

                             M  S  E  N  S  E  P  R  Q  L  E  N  S  T  -

     GCCGGAAGAGAGCTCATTCCTCTTAGTCCCACCAATTCAGACGGCAACGACGACCTTAAC
 61  ---------+---------+---------+---------+---------+---------+ 120
     CGGCCTTCTCTCGAGTAAGGAGAATCAGGGTGGTTAAGTCTGCCGTTGCTGCTGGAATTG

     A  G  R  E  L  L  P  L  S  P  T  N  S  D  G  N  D  D  L  N  -

     TATCATCTGCATGCTTTTGAGTTATCTCGTCTCCTACTTTCTTCTGGTCATCCAGAATCT
121  ---------+---------+---------+---------+---------+---------+ 180
     ATAGTAGACGTACGAAAACTCAATAGAGCAGAGGATGAAAGAAGACCAGTAGGTCTTAGA

     Y  H  L  H  A  F  E  L  S  R  L  L  L  S  S  G  H  P  E  S  -

     GTTATAGATCTTTCTTCAAAGTGTACATACTTCCAAGGTTCTCCTAATCTCGTCAAATAT
181  ---------+---------+---------+---------+---------+---------+ 240
     CAATATCTAGAAAGAAGTTTCACATGTATGAAGGTTCCAAGAGGATTAGAGCAGTTTATA

     V  I  D  L  S  S  K  C  T  Y  F  Q  G  S  P  N  L  V  K  Y  -

     CTTTGCTCGATCCCTAATTCTCCTATTTCCCTTGCCGAAGATGGCTTCACTGTGACTCTC
241  ---------+---------+---------+---------+---------+---------+ 300
     GAAACGAGCTAGGGATTAAGAGGATAAAGGGAACGGCTTCTACCGAAGTGACACTGAGAG

     L  C  S  I  P  N  S  P  I  S  L  A  E  D  G  F  T  V  T  L  -

     TCGCCTGAGTCTCCCTCCGCTCCGGCTAGTTTCGCCTGTAGTTTGGATTTGCAGGAAAAT
301  ---------+---------+---------+---------+---------+---------+ 360
     AGCGGACTCAGAGGGAGGCGAGGCCGATCAAAGCGGACATCAAACCTAAACGTCCTTTTA

     S  P  E  S  P  S  A  P  A  S  F  A  C  S  L  D  L  Q  E  N  -

                                                           1  2
     GTTGTGTTAGAACAGTTTATGGATCCGAGATCTCTCACGCTAAAGCATTCGAGAGAGAAT
361  ---------+---------+---------+---------+---------+---------+ 420
     CAACACAATCTTGTCAAATACCTAGGCTCTAGAGAGTGCGATTTCGTAAGCTCTCTCTTA
                                                           1  2
     V  V  L  E  Q  F  M  D  P  R  S  L  T  L  K  H  S  R  E  N  -

     GCGGAACAAGAGGAGCTAGAGCTCATGCCATTGCCCAAAAGAAGTCGAAATGATGGAAAC
421  ---------+---------+---------+---------+---------+---------+ 480
     CGCCTTGTTCTCCTCGATCTCGAGTACGGTAACGGGTTTTCTTCAGCTTTACTACCTTTG

     A  E  Q  E  E  L  E  L  M  P  L  P  K  R  S  R  N  D  G  N  -
```

43

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          GATGTGAATTACTCTGTAATAGTAGCAGACCTAACGACATCAGAACTGTTGCCTGTGGA
481       ------------------------------------------------------------ 540
          CTACACTTAATGAGACATTATCTATCGTCTGGATTGCTGTAGTCTTGACAACGGACACCT
                43
           D | V  N  Y  S  V  I  D  S  R  E  N  D  I  R  T  V  A  C  G  -

          ACTATGCTTGGGACTATTTTAGCTCTTGAATCCCAAGCTTCGGTTTTCAATTTAAGTGCA
541       ------------------------------------------------------------ 600
          TGATACGAACCCTGATAAAATCGAGAACTTAGGGTTCGAAGCCAAAAGTTAAATTCACGT
           T  M  L  G  T  I  L  A  L  E  S  Q  A  S  V  F  N  L  S  A  -

          TCTAACCGAGGAATAGAGGCTTTTGTTCAAGATCATCAGCCTGGTCCGCAGACATCCAAT
601       ------------------------------------------------------------ 660
          AGATTGGCTCCTTATCTCCGAAAACAAGTTCTAGTAGTCGGACCAGGCGTCTGTAGGTTA
           S  N  R  G  I  E  A  F  V  Q  D  H  Q  P  G  P  Q  T  S  N  -

          GCTTCAGTGGATGTCAATCCTACACATCGGTTAGAGGAAAGCAAGAACGATTTGCCATCT
661       ------------------------------------------------------------ 720
          CGAAGTCACCTACAGTTAGGATGTGTAGCCAATCTCCTTTCGTTCTTGCTAAACGGTAGA
           A  S  V  D  V  N  P  T  H  R  L  E  E  S  K  N  D  L  P  S  -

          CCTCAGGAGGATGGATATTACGAGCGACCTGAAATTGGAGATTTCCAAATTGCTGACAAC
721       ------------------------------------------------------------ 780
          GGAGTCCTCCTACCTATAATGCTCGCTGGACTTTAACCTCTAAAGGTTTAACGACTGTTG
           P  Q  E  D  G  Y  Y  E  R  P  E  I  G  D  F  Q  I  A  D  N  -

          CAAATATTAATCGAAGAAGGTGATGATAAAAATAAGAAGGATCTCTTCCCTAAGGGAGAG
781       ------------------------------------------------------------ 840
          GTTTATAATTAGCTTCTTCCACTACTATTTTTATTCTTCCTAGAGAAGGGATTCCCTCTC
           Q  I  L  I  E  E  G  D  D  K  N  K  K  D  L  F  P  K  G  E  -

          ATACAAACTGATTCTGTGCAGTCCGATCCCGTTGCCTCATTGATGCCAACAGAAAATGAG
841       ------------------------------------------------------------ 900
          TATGTTTGACTAAGACACGTCAGGCTAGGGCAACGGAGTAACTACGGTTGTCTTTTACTC
           I  Q  T  D  S  V  Q  S  D  P  V  A  S  L  M  P  T  E  N  E  -

          TTAGAACCAGTGCAGATTGTGGATGACACTGAAGATCTACTTGTAGATGATCACACTGTA
901       ------------------------------------------------------------ 960
          AATCTTGGTCACGTCTAACACCTACTGTGACTTCTAGATGAACATCTACTAGTGTGACAT
           L  E  P  V  Q  I  V  D  D  T  E  D  L  L  V  D  D  H  T  V  -

          GACATCGTTAGCACCCCTGACAGAGAGCTGCCGTTGAAGCCTTCTGCTACAGAAGCTAAT
961       ------------------------------------------------------------ 1020
          CTGTAGCAATCGTGGGGACTGTCTCTCGACGGCAACTTCGGAAGACGATGTCTTCGATTA
           D  I  V  S  T  P  D  R  E  L  P  L  K  P  S  A  T  E  A  N  -

          CAAGATAAATCTTTGGTACAAAAAACTCTGGATCAATGCAAATTGCCGGGAAACAGCAAA
1021      ------------------------------------------------------------ 1080
          GTTCTATTTAGAAACCATGTTTTTTGAGACCTAGTTACGTTTAACGGCCCTTTGTCGTTT
```

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        Q  D  K  S  L  V  Q  K  T  L  D  Q  C  K  L  E  G  N  S  K    -

       ACGTACAGCTGTTCCCCTGAGATAAAACACACCAGAAAAGTAAAGTTATCCAGAAGAGG
1081   --------+---------+---------+---------+---------+---------+  1140
       TGCATGTCGACAAGGGGACTCTATTTTGTGTGGTCTTTTCATTTCAATAGGTCTTCTCC

        T  Y  S  C  S  P  E  I  K  E  T  R  K  S  K  V  I  Q  K  R    -
                                            3|4
       AAGCAGAATTTTAACACCGTTCGTCTTAAAGATCAGAAGATCAGGCAAAGCATAACACA
1141   --------+---------+---------+---------+---------+---------+  1200
       TTCGTCTTAAAATTGTGGCAAGCAGAATTTCTAGTCTTCCTAGTCCGTTTCGTATTGTGT

        K  Q  N  F  N  T  V  R  L  K  D  Q  K  D  Q  A  K  E  N  T    -
                                         3|4              4|5
       ATTCCAGATTTTGATTCTTACACTATTGTAGAGGAAGAAGGTTCAGGTGGCTACGGGATT
1201   --------+---------+---------+---------+---------+---------+  1260
       TAAGGTCTAAAACTAAGAATGTGATAACATCTCCTTCTTCCAAGTCCACCGATGCCCTAA

        I  P  D  F  D  S  Y  T  I  V  E  E  E  G  S  G  G  Y  G  I    -
                                               4|5
                                               5|6
       GTTTATAAGGCAACGAGGAAAACTGATGGAACAGAGTTTGCAATTAAATGCCCTCATGTT
1261   --------+---------+---------+---------+---------+---------+  1320
       CAAATATTCCGTTGCTCCTTTTGACTACCTTGTCTCAAACGTTAATTTACGGGAGTACAA
                                               5|6

        V  Y  K  A  T  R  K  T  D  G  T  E  F  A  I  K  C  P  H  V    -
                                               5|6             6|7
       GGCGCTCAGAAGTATTATGTGAATAATGAAATCAGAATGCTGGAGCGTTTTGGGGGGAAA
1321   --------+---------+---------+---------+---------+---------+  1380
       CCGCGAGTCTTCATAATACACTTATTACTTTAGTCTTACGACCTCGCAAAACCCCCCTTT
                                                               6|7

        G  A  Q  K  Y  Y  V  N  N  E  I  R  M  L  E  R  F  G  G  K    -
                                                             6|7
       AACTGTATAATAAAGCATGAAGGCTGTCTCAAGAATGGAGATTCTGATTGCATCATCCTT
1381   --------+---------+---------+---------+---------+---------+  1440
       TTGACATATTATTTCGTACTTCCGACAGAGTTCTTACCTCTAAGACTAACGTAGTAGGAA

        N  C  I  I  K  H  E  G  C  L  K  N  G  D  S  D  C  I  L       -

       GAGCACCTTGAACATGACAGACCTGATTCATTGAAGAGAGAAATAGATGTGTATCAGCTG
1441   --------+---------+---------+---------+---------+---------+  1500
       CTCGTGGAACTTGTACTGTCTGGACTAAGTAACTTCTCTCTTTATCTACACATAGTCGAC

        E  H  L  E  H  D  R  P  D  S  L  K  R  E  I  D  V  Y  Q  L    -
                                                      7|8
       CAGTGGTACGGCTACTGCATGTTCAAAGCTCTATCGAGTCTGCATAAGCAGGGTGTTGTT
1501   --------+---------+---------+---------+---------+---------+  1560
       GTCACCATGCCGATGACGTACAAGTTTCGAGATAGCTCAGACGTATTCGTCCCACAACAA

        Q  W  Y  G  Y  C  M  F  K  A  L  S  S  L  H  K  Q  G  V  V    -
                                                      7|8
       CATAGGGATGTTAAGCCAGGAAACTTCCTCTTCTCTAGGAAGACCAACAAAGGCTATCTC
1561   --------+---------+---------+---------+---------+---------+  1620
       GTATCCCTACAATTCGGTCCTTTGAAGGAGAAGAGATCCTTCTGGTTGTTTCCGATAGAG

        H  R  D  V  K  P  G  N  F  L  F  S  R  K  T  N  K  G  Y  L    -
                               8|9                    9|10
       ATTGATTTTAACCTTGCCATGGATTTGCACCAGAAGTACAGAAGAGCAGATAAATCAAAA
```

```
1621 ------------+---------+---------+---------+---------+--------+ 1680
     TAACTAAAATTGGAACGGTACCTAAACGTGGTCTTCATGTCTTCCGTCTATTTAGTTTT
                           8│9                            9│70
     I  D  F  N  L  A  M │ D  L  H  Q  K  Y  R  R  A  D │ K  S  K   -

     GCAGCTTCAGGTCTTCCTACCGCCAGCAAGAAACATCATACATTGGTTAAATCACTCGAT
1681 ------------+---------+---------+---------+---------+--------+ 1740
     CGTCGAAGTCCAGAAGGATGGCGGTCGTTCTTTGTAGTATGTAACCAATTTAGTGAGCTA
     A  A  S  G  L  P  T  A  S  K  K  H  E  T  L  V  K  S  L  D   -

     GCGGTAAACCGAGGGACCAACAAACCTTCTCAGAAACTTTAGCGCCTAATAGTATCAAG
1741 ------------+---------+---------+---------+---------+--------+ 1800
     CGCCATTTGGCTCCCTGGTTGTTTGGAAGAGTCTTTGAAATCGCGGATTATCATAGTTC
     A  V  N  R  G  T  N  K  P  S  Q  K  T  L  A  P  N  S  I  K   -

     AAAGCAGCGGGAAAGACAAGAGCTCGGAATGACATGACCAGATGGGAGAGACTCAATAGC
1801 ------------+---------+---------+---------+---------+--------+ 1860
     TTTCGTCGCCCTTTCTGTTCTCGAGCCTTACTGTACTGGTCTACCCTCTCTGAGTTATCG
     K  A  A  G  K  T  R  A  R  N  D  M  T  R  W  E  R  L  N  S   -

     CAAGGGGCAGAAGGGTCTGGCTTAACTTCAGCTAAAGATGTGACCAGCACAAGGAACAAC
1861 ------------+---------+---------+---------+---------+--------+ 1920
     GTTCCCCGTCTTCCCAGACCGAATTGAAGTCGATTTCTACACTGGTCGTGTTCCTTGTTG
     Q  G  A  E  G  S  G  L  T  S  A  K  D  V  T  S  T  R  N  N   -

     CCTTCAGGTGAAAAGAGAAGAGAGCCTTTGCCATGTCATGGAAGAAAAGCGCTTTTAGAT
1921 ------------+---------+---------+---------+---------+--------+ 1980
     GGAAGTCCACTTTTCTCTTCTCTCGGAAACGGTACAGTACCTTCTTTTCGCGAAAATCTA
     P  S  G  E  K  R  R  E  P  L  P  C  H  G  R  K  A  L  L  D   -

     TTTCTGCAAGAGACAATGTCTGTTCCAATTCCAAACCATGAAGTATCATCCAAAGCTCCT
1981 ------------+---------+---------+---------+---------+--------+ 2040
     AAAGACGTTCTCTGTTACAGACAAGGTTAAGGTTTGGTACTTCATAGTAGGTTTCGAGGA
     F  L  Q  E  T  M  S  V  P  I  P  N  H  E  V  S  S  K  A  P   -

     ACGTCTATGAGAAAACGGGTAGCTGCTCTTCCAGGGAAAGCTGAGAAGGAACTTCTTTAT
2041 ------------+---------+---------+---------+---------+--------+ 2100
     TGCAGATACTCTTTTGCCCATCGACGAGAAGGTCCCTTTCGACTCTTCCTTGAAGAAATA
     T  S  M  R  K  R  V  A  A  L  P  G  K  A  E  K  E  L  L  Y   -

                                                   10│11
     CTGACCCCAATGCCACTGTGCTCTAACGGTCGGCCTGAAGCAGGGGACGTAATTGAGAAG
2101 ------------+---------+---------+---------+---------+--------+ 2160
     GACTGGGGTTACGGTGACACGAGATTGCCAGCCGGACTTCGTCCCCTGCATTAACTCTTC
                                                   10│11
     L  T  P  M  P  L  C  S  N  G  R  P  E  A  G │ D  V  I  E  K   -

                                                   11│12
     AAAGACGGTCCTTGCTCAGGAACCAAAGGCTTCCGAGCTCCAGAGGTTTGCTTCAGATCT
2161 ------------+---------+---------+---------+---------+--------+ 2220
     TTTCTGCCAGGAACGAGTCCTTGGTTTCCGAAGGCTCGAGGTCTCCAAACGAAGTCTAGA
                                                   11│12
     K  D  G  P  C  S  G  T  K  G  F  R  A  P  E │ V  C  F  R  S   -
```

```
2221 TTGCACCAAGGACCTAAGATAGACGTGTGGTCTGCGGGAGTTACTTTGTTATACCTCATA 2280
     ------------+---------+---------+---------+---------+--------
     AACGTGGTTCCTGGATTCTATCTGCACACCAGACGCCCTCAATGAAACAATATGGAGTAT

      L  H  Q  G  E  K  L  D  V  W  S  A  G  V  T  L  L  Y  L  L  -

                                              12|13
2281 ATGGAAGGACACCTTTCACTGGTGACCCTGAACAGAACATAAAGGACATTGCACAACTA 2340
     ------------+---------+---------+---------+---------+--------
     TACCCTTCCTGTGGAAAGTGACCACTGGGACTTGTCTTGTATTTCCTGTAACGTGTTGAT
                                              12|13
      M  G  R  T  P  F  T  G  D  E  Q  N  I  K  D  I  A  Q  L  -

2341 CGAGGCAGTGAAGAATTATGGGAAGTAGCCAAGCTGCACAACCGTGAATCCTCTTTCCCT 2400
     ------------+---------+---------+---------+---------+--------
     GCTCCGTCACTTCTTAATACCCTTCATCGGTTCGACGTGTTGGCACTTAGGAGAAAGGGA

      R  G  S  E  L  W  E  V  A  K  L  H  N  R  E  S  S  F  P  -

        13|14
2401 AAGGAATTATACGAGTCAAGGTACTTGAAGGGGATGGAGTTGAGAAAATGGTGCGAACTC 2460
     ------------+---------+---------+---------+---------+--------
     TTCCTTAATATGCTCAGTTCCATGAACTTCCCCTACCTCAACTCTTTTACCACGCTTGAG
        13|14
      K  E  L  Y  E  S  R  Y  L  K  G  M  E  L  R  K  W  C  E  L  -

2461 AACACAAAACGCAGAGAGTTTCTAGACGTAATTCCACTATCGCTTCTTGACCTCGTTGAT 2520
     ------------+---------+---------+---------+---------+--------
     TTGTGTTTTGCGTCTCTCAAAGATCTGCATTAAGGTGATAGCGAAGAACTGGAGCAACTA

      N  T  K  R  R  E  F  L  D  V  I  P  L  S  L  L  D  L  V  D  -

2521 AAATGTTTGACCGTTAACCCGAGGCGACGAATCAGCGCAGAGGATGCTCTCAAGCACGAC 2580
     ------------+---------+---------+---------+---------+--------
     TTTACAAACTGGCAATTGGGCTCCGCTGCTTAGTCGCGTCTCCTACGAGAGTTCGTGCTG

      K  C  L  T  V  N  P  R  R  R  I  S  A  E  D  A  L  K  H  D  -

2581 TTCTTCCATCCAGTACATGAAACCCTTAGAAACCAAATGCTCCTTAAACAGCAGCCTACA 2640
     ------------+---------+---------+---------+---------+--------
     AAGAAGGTAGGTCATGTACTTTGGGAATCTTTGGTTTACGAGGAATTTGTCGTCGGATGT

      F  F  H  P  V  H  E  T  L  R  N  Q  M  L  L  K  Q  Q  P  T  -

                                                        14|
2641 GTGGTTGCTGACGCAGTAAGCCAAACTCTAAACTATTTACAATTGTAAAAGTAAATAAG 2699
     ------------+---------+---------+---------+---------+--------
     CACCAACGACTGCGTCATTCGGTTTGAGATTTGATAAATGTTAACATTTTCATTTATTC

      V  V  A  D  A  V  S  Q  T  L  N  Y  L  Q  L  *
```

Fig. 4

```
1   ------------+----------+----------+----------+----------+----------+   60
    CCGCTGTAATGTGTGTGTCGGAGGCTCCTTGTTGTTGTTGTAGCTAACAGAGCAGTTAAA

                                         |1
                                         |ATGATGGAGAATCTACTGGCGAATTGTGTCCAGAAAAACCTT
61  ------------+----------+----------+----------+----------+----------+   120
    CCAGTAGTAGTAGTAGTCTACTACCTCTTAGATGACCGCTTAACACAGGTCTTTTTGGAA
                                         |1
                                          M   M   E   N   L   L   A   N   C   V   Q   K   N   L

    AACCATTTTATGTTCACCAATGCTATCTTCCTTTGCGAACTTCTTCTCGCCCAATTTCCA
121 ------------+----------+----------+----------+----------+----------+   180
    TTGGTAAAATACAAGTGGTTACGATAGAAGGAAACGCTTGAAGAAGAGCGGGTTAAAGGT
      N   H   F   M   F   T   N   A   I   F   L   C   E   L   L   A   Q   F   P

         1|2
    TCTGAGGTGAACCTGCAATTGTTAGCCAGGTGTTACTTGAGTAACAGTCAAGCTTATAGT
181 ------------+----------+----------+----------+----------+----------+   240
    AGACTCCACTTGGACGTTAACAATCGGTCCACAATGAACTCATTGTCAGTTCGAATATCA
      S   E |1|2 V   N   L   Q   L   L   A   R   C   Y   L   S   N   S   Q   A   Y   S

                         2|3
    GCATATTATATCCTTAAAGGTTCAAAAACGCCTCAGTCTCGGTATTTATTTGCATTCTCA
241 ------------+----------+----------+----------+----------+----------+   300
    CGTATAATATAGGAATTTCCAAGTTTTTGCGGAGTCAGAGCCATAAATAAACGTAAGAGT
      A   Y   Y   I   L   K |2|3 G   S   K   T   P   Q   S   R   Y   L   F   A   F   S

    TGCTTTAAGTTGGATCTTCTTGGAGAGGCTGAAGCTGCATTGTTGCCCTGTGAAGATTAT
301 ------------+----------+----------+----------+----------+----------+   360
    ACGAAATTCAACCTAGAAGAACCTCTCCGACTTCGACGTAACAACGGGACACTTCTAATA
      C   F   K   L   D   L   L   G   E   A   E   A   A   L   L   P   C   E   D   Y

         3|4                                                          4|5
    GCTGAAGAAGTTCCTGGTGGTGCAGCTGGGCATTATCTTCTTGGTCTTATATATAGATAT
361 ------------+----------+----------+----------+----------+----------+   420
    CGACTTCTTCAAGGACCACCACGTCGACCCGTAATAGAAGAACCAGAATATATATCTATA
      A   E   E |3|4 V   P   G   G   A   A   G   H   Y   L   L   G   L   I   Y   R |4|5 Y
```

```
     TCTGGGAGGAAGAACTGTTCAATACAACAGTTTAGGATGGCATTGTCATTTGATCCATTG
421  --------+---------+---------+---------+---------+---------+ 480
     AGACCCTCCTTCTTGACAAGTTATGTTGTCAAATCCTACCGTAACAGTAAACTAGGTAAC

       S  G  R  K  N  C  S  I  Q  Q  F  R  M  A  L  S  F  D  P  L
                                         5|6
     TGTTGGGAAGCATATGGAGAACTTTGTAGTTTAGGTGCCGCTGAAGAAGCCTCAACAGTT
481  --------+---------+---------+---------+---------+---------+ 540
     ACAACCCTTCGTATACCTCTTGAAACATCAAATCCACGGCGACTTCTTCGGAGTTGTCAA

       C  W  E  A  Y  G  E  L  C  S  L  G |A  A  E  E  A  S  T  V
                                        5|6
     TTCGGGAATGTTGCTTCCCAGCGTCTTAAAACTTGTGTAGAACAAAGAATAAGCTTCTCA
541  --------+---------+---------+---------+---------+---------+ 600
     AAGCCCTTACAACGAAGGGTCGCAGAATTTTGAACACATCTTGTTTCTTATTCGAAGAGT

       F  G  N  V  A  S  Q  R  L  K  T  C  V  E  Q  R  I  S  F  S

     GAAGGAGCAACCATAGACCAGATTACAGATTCTGATAAGGCCTTAAAAGATACAGGTTTA
601  --------+---------+---------+---------+---------+---------+ 660
     CTTCCTCGTTGGTATCTGGTCTAATGTCTAAGACTATTCCGGAATTTTCTATGTCCAAAT

       E  G  A  T  I  D  Q  I  T  D  S  D  K  A  L  K  D  T  G  L

     TCGCAAACAGAACACATTCCAGGAGAGAACCAACAAGATCTGAAAATTATGCAGCAGCCT
661  --------+---------+---------+---------+---------+---------+ 720
     AGCGTTTGTCTTGTGTAAGGTCCTCTCTTGGTTGTTCTAGACTTTTAATACGTCGTCGGA

       S  Q  T  E  H  I  P  G  E  N  Q  Q  D  L  K  I  M  Q  Q  P

     GGAGATATTCCACCAAATACTGACAGGCAACTTAGTACAAACGGATGGGACTTGAACACA
721  --------+---------+---------+---------+---------+---------+ 780
     CCTCTATAAGGTGGTTTATGACTGTCCGTTGAATCATGTTTGCCTACCCTGAACTTGTGT

       G  D  I  P  P  N  T  D  R  Q  L  S  T  N  G  W  D  L  N  T
                               6|7
     CCTTCTCCAGTGCTTTTACAGGTAATGGATGCTCCACCGCCTCTGCTTCTTAAGAATATG
781  --------+---------+---------+---------+---------+---------+ 840
     GGAAGAGGTCACGAAAATGTCCATTACCTACGAGGTGGCGGAGACGAAGAATTCTTATAC
                              6|7
       P  S  P  V  L  L  Q  V |M  D  A  P  P  P  L  L  L  K  N  M

     CGTCGTCCAGCAGTGGAAGGATCTTTGATGTCTGTACATGGAGTGCGTGTGCGTCGAAGA
841  --------+---------+---------+---------+---------+---------+ 900
     GCAGCAGGTCGTCACCTTCCTAGAAACTACAGACATGTACCTCACGCACACGCAGCTTCT

       R  R  P  A  V  E  G  S  L  M  S  V  H  G  V  R  V  R  R  R
```

```
                                                  7 8
     AACTTTTTTAGTGAAGAATTGTCAGCAGAGGCTCAAGAAGAATCTGGGCGCCGCCGTAGT
901  ---------+---------+---------+---------+---------+---------+  960
     TTGAAAAAATCACTTCTTAACAGTCGTCTCCGAGTTCTTCTTAGACCCGCGGCGGCATCA
                                                  7 8
      N  F  F  S  E  E  L  S  A  E | A  Q  E  E  S  G  R  R  R  S

      GCTAGAATAGCAGCAAGGAAAAAGAATCCTATGTCGCAGTCATTTGGAAAAGATTCCCAT
961   ---------+---------+---------+---------+---------+---------+ 1020
      CGATCTTATCGTCGTTCCTTTTTCTTAGGATACAGCGTCAGTAAACCTTTTCTAAGGGTA

       A  R  I  A  A  R  K  K  N  P  M  S  Q  S  F  G  K  D  S  H

      TGGTTACATCTTTCACCTTCCGAGTCAAACTATGCACCTTCTCTTTCCTCGATGATTGGA
1021  ---------+---------+---------+---------+---------+---------+ 1080
      ACCAATGTAGAAAGTGGAAGGCTCAGTTTGATACGTGGAAGAGAAAGGAGCTACTAACCT

       W  L  H  L  S  P  S  E  S  N  Y  A  P  S  L  S  S  M  I  G
                               8 9
      AAATGCAGAATCCAAAGCAGCAAAGAAGCGATTCCTGATACCGTTACTCTAAATGATCCA
1081  ---------+---------+---------+---------+---------+---------+ 1140
      TTTACGTCTTAGGTTTCGTCGTTTCTTCGCTAAGGACTATGGCAATGAGATTTACTAGGT
                               8 9
       K  C  R  I  Q  S  S  K  E  A | I  P  D  T  V  T  L  N  D  P

      GCAACGACGTCAGGCCAGTCTGTAAGTGACACTGGAAGCTCTGTTGATGATGAGGAAAAG
1141  ---------+---------+---------+---------+---------+---------+ 1200
      CGTTGCTGCAGTCCGGTCAGACATTCACTGTGACCTTCGAGACAACTACTACTCCTTTTC

       A  T  T  S  G  Q  S  V  S  D  T  G  S  S  V  D  D  E  K

      TCAAATCCTAGTGAATCTTCCCCGGATCGTTTCAGCCTTATTTCTGGAATTTCAGAAGTG
1201  ---------+---------+---------+---------+---------+---------+ 1260
      AGTTTAGGATCACTTAGAAGGGGCCTAGCAAAGTCGGAATAAAGACCTTAAAGTCTTCAC

       S  N  P  S  E  S  S  P  D  R  F  S  L  I  S  G  I  S  E  V
                                                                9
      CTAGGCATTCTGAAAATTCTTGGAGATGGCCACAGGCATTTACATATGTACAAGTGTCAG
1261  ---------+---------+---------+---------+---------+---------+ 1320
      GATCCGTAAGACTTTTAAGAACCTCTACCGGTGTCCGTAAATGTATACATGTTCACAGTC
                                                                9
       L  G  I  L  K  I  L  G  D  G  H  R  H  L  H  M  Y  K  C  Q |
```

```
       |10
      GAAGCTTTGTTGGCATATCAAAAGCTATCTCAGAAACAATACAATACACACTGGGTTCTC
1321  ---------+---------+---------+---------+---------+---------+  1380
      CTTCGAAACAACCGTATAGTTTTCGATAGAGTCTTTGTTATGTTATGTGTGACCCAAGAG
       |10
       |E  A  L  L  A  Y  Q  K  L  S  Q  K  Q  Y  N  T  H  W  V  L
          10|11
      ATGCAGGTTGGAAAAGCATATTTTGAGCTACAAGACTACTTCAACGCTGACTCTTCCTTT
1381  ---------+---------+---------+---------+---------+---------+  1440
      TACGTCCAACCTTTTCGTATAAAACTCGATGTTCTGATGAAGTTGCGACTGAGAAGGAAA
          10|11
       M  Q| V  G  K  A  Y  F  E  L  Q  D  Y  F  N  A  D  S  S  F
      ACTCTTGCTCATCAAAAGTATCCTTATGCTTTGGAAGGAATGGATACATACTCCACTGTT
1441  ---------+---------+---------+---------+---------+---------+  1500
      TGAGAACGAGTAGTTTTCATAGGAATACGAAACCTTCCTTACCTATGTATGAGGTGACAA
       T  L  A  H  Q  K  Y  P  Y  A  L  E  G  M  D  T  Y  S  T  V
          11|12
      CTTTATCACCTGAAAGAAGAGATGAGGTTGGGCTATCTGGCTCAGGAACTGATTTCAGTT
1501  ---------+---------+---------+---------+---------+---------+  1560
      GAAATAGTGGACTTTCTTCTCTACTCCAACCCGATAGACCGAGTCCTTGACTAAAGTCAA
          11|12
       L  Y| H  L  K  E  E  M  R  L  G  Y  L  A  Q  E  L  I  S  V
                 12|13
      GATCGCCTGTCTCCAGAATCCTGGTGTGCAGTTGGGAACTGTTACAGTTTGCGTAAGGAT
1561  ---------+---------+---------+---------+---------+---------+  1620
      CTAGCGGACAGAGGTCTTAGGACCACACGTCAACCCTTGACAATGTCAAACGCATTCCTA
                 12|13
       D  R  L  S  P  E  S  W| C  A  V  G  N  C  Y  S  L  R  K  D
      CATGATACTGCTCTCAAAATGTTTCAGAGAGCTATCCAACTGAATGAAAGATTCACATAT
1621  ---------+---------+---------+---------+---------+---------+  1680
      GTACTATGACGAGAGTTTTACAAAGTCTCTCGATAGGTTGACTTACTTTCTAAGTGTATA
       H  D  T  A  L  K  M  F  Q  R  A  I  Q  L  N  E  R  F  T  Y
                13|14
      GCACATACCCTTTGTGGCCACGAGTTTGCCGCATTGGAAGAATTCGAGGATGCAGAGAGA
1681  ---------+---------+---------+---------+---------+---------+  1740
      CGTGTATGGGAAACACCGGTGCTCAAACGGCGTAACCTTCTTAAGCTCCTACGTCTCTCT
                13|14
       A  H  T  L  C  G  H  E| F  A  A  L  E  E  F  E  D  A  E  R
      TGCTACCGGAAGGCTCTGGGCATAGATACGAGACACTATAATGCATGGTACGGTCTTGGA
1741  ---------+---------+---------+---------+---------+---------+  1800
      ACGATGGCCTTCCGAGACCCGTATCTATGCTCTGTGATATTACGTACCATGCCAGAACCT
       C  Y  R  K  A  L  G  I  D  T  R  H  Y  N  A  W  Y  G  L  G  -
```

```
      ATGACCTATCTTCGTCAGGAGAAATTCGAGTTTGCGCAGCATCAATTTCAACTGGCTCTC
1801  ---------+---------+---------+---------+---------+---------+  1860
      TACTGGATAGAAGCAGTCCTCTTTAAGCTCAAACGCGTCGTAGTTAAAGTTGACCGAGAG

       M  T  Y  L  R  Q  E  K  F  E  F  A  Q  H  Q  F  Q  L  A  L

      CAAATAAATCCAAGATCTTCAGTCATCATGTGTTACTATGGAATTGCTTTGCATGAGTCA
1861  ---------+---------+---------+---------+---------+---------+  1920
      GTTTATTTAGGTTCTAGAAGTCAGTAGTACACAATGATACCTTAACGAAACGTACTCAGT

       Q  I  N  P  R  S  S  V  I  M  C  Y  Y  G  I  A  L  H  E  S
                                                                14|15
      AAGAGAAACGATGAGGCGTTGATGATGATGGAGAAGGCTGTACTCACTGATGCAAAGAAT
1921  ---------+---------+---------+---------+---------+---------+  1980
      TTCTCTTTGCTACTCCGCAACTACTACTACCTCTTCCGACATGAGTGACTACGTTTCTTA
        14|15
       K |R  N  D  E  A  L  M  M  M  E  K  A  V  L  T  D  A  K  N

      CCGCTCCCCAAGTACTACAAGGCTCACATATTAACCAGCCTAGGTGATTATCACAAAGCA
1981  ---------+---------+---------+---------+---------+---------+  2040
      GGCGAGGGGTTCATGATGTTCCGAGTGTATAATTGGTCGGATCCACTAATAGTGTTTCGT

       P  L  P  K  Y  Y  K  A  H  I  L  T  S  L  G  D  Y  H  K  A

      CAGAAAGTTTTAGAAGAGCTCAAAGAATGTGCTCCTCAAGAAAGCAGTGTCCATGCATCG
2041  ---------+---------+---------+---------+---------+---------+  2100
      GTCTTTCAAAATCTTCTCGAGTTTCTTACACGAGGAGTTCTTTCGTCACAGGTACGTAGC

       Q  K  V  L  E  E  L  K  E  C  A  P  Q  E  S  S  V  H  A  S

      CTTGGCAAAATATACAATCAGCTAAAGCAATACGACAAAGCCGTGTTACATTTCGGCATT
2101  ---------+---------+---------+---------+---------+---------+  2160
      GAACCGTTTTATATGTTAGTCGATTTCGTTATGCTGTTTCGGCACAATGTAAAGCCGTAA

       L  G  K  I  Y  N  Q  L  K  Q  Y  D  K  A  V  L  H  F  G  I
                                                        15|16
      GCTTTGGATTTAAGCCCTTCTCCATCTGATGCTGTCAAGATAAAGGCTTACATGGAGAGG
2161  ---------+---------+---------+---------+---------+---------+  2220
      CGAAACCTAAATTCGGGAAGAGGTAGACTACGACAGTTCTATTTCCGAATGTACCTCTCC
                                                        15|16
       A  L  D  L  S  P  S  P  S  D  A  V  K  I  K |A  Y  M  E  R
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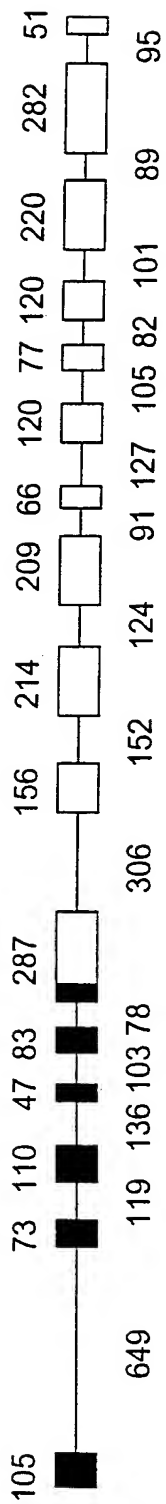
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                                                     161
                                                      |
     TTGATACTACCAGACGAGCTGGTGACGGAGGAAAATTTGTAGATTTATTGTGCAGGTAAT
2221 ------------+---------+---------+---------+---------+---------  2280
     AACTATGATGGTCTGCTCGACCACTGCCTCCTTTTAAACATCTAAATAACACGTCCATTA

        L  L  L  P  D  E  L  V  T  E  E  N  L  *   .    .    .    .

     ACACCAGATTATGTTTCTCATATAACCCAAAGTCATCTGTAATTTTTCTCATCTTTAGAT
2281 ------------+---------+---------+---------+---------+---------  2340
     TGTGGTCTAATACAAAGAGTATATTGGGTTTCAGTAGACATTAAAAAGAGTAGAAATCTA

         .    .    .    .    .    .    .    .    .    .    .

     CAGTCTTGTGGACTAACCCTAAAACAAAACTGATTATATAAACTTAGAGGGTAATATTAC
2341 ------------+---------+---------+---------+---------+---------  2400
     GTCAGAACACCTGATTGGGATTTTGTTTTGACTAATATATTTGAATCTCCCATTATAATG

         .    .    .    .    .    .    .    .    .    .    .

     AGAAAATTGTATAGAGTTGGGTTTGAATTTTCATTTCTTTTCCAAGTTGGAACTTTTGTT
2401 ------------+---------+---------+---------+---------+---------  2460
     TCTTTTAACATATCTCAACCCAAACTTAAAAGTAAAGAAAAGGTTCAACCTTGAAAACAA

         .    .    .    .    .    .    .    .    .    .    .

     CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
2461 ------------+---------+---------+---------+---------+---  2512
     GTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

         .    .    .    .    .    .    .    .    .    .    .
```

CDC27B Gene Structure

105		73	110	47	83	287		156	214	209	66	120	77	120	220	282	51
	649		119	136	103	78	306		152	124		91	127	105	82	101	89	95

FIGURE 5

                                                              SEQ ID NO 6
Cdc27A1   1- MMENLLANCVQKNLNHFMFTNAIFLCELLLAQFPSEVNLQLLARCYLSNS
Cdc27B   1- MEAMLV-DCVNNSLRHFVYKNAIFMCERLCAEFPSEVNLQLLATSYLQNN
                                  SEQ ID NO 10

              SEQ ID NO 6
Cdc27A1   51- QAYSAYYILKGSKTPQSRYLFAFSCFKLDLLGEAEAALLP-CEDYAEEVP
Cdc27B   50- QAYSAYHLLKGTQMAQSRYLFALSCFQMDLLNEAESALCPVNEPGAE-IP
                                  SEQ ID NO 10

Cdc27A1 100- GGAAGHYLLGLIYRYSGRKNCSIQQFRMALSFDPLCWEAYGELCSLGAAE
Cdc27B   99- NGAAGHYLLGLIY----KKNAA-QQFKQSLTIDPLLWAAYEELCILGAAE
                                  SEQ ID NO 10

Cdc27A1 150- EASTVFGNVASQRLQKTCVEQRISFSEG-ATIDQ--ITDSDKAL--KDTG
Cdc27B   144- EATAVFGETAALSIQKQYMQQ-LSTSLGLNTYNEERNSTSTKNTSSEDYS
                     SEQ ID NO 10

Cdc27A1 194- LSQTEHIPGENQQDLKIMQQPGDIPPNTDRQLSTNGWDLNTPSPVLLQVM
Cdc27B   193- PRQSKHTQSHGLKDISGNFHSHGVNGGV----SNMSFY-NTPSPVAAQLS

Cdc27A1 244- D-APPPLLL NMRRPAV-EG-SLMS-------VHG-VRVRRRNFFSE---
Cdc27B   238- GIAPPPL-FRNFQ-PAVANPNSLITDSSPKSTVNSTLQAPRRKFVDEGKL

Cdc27A1 280- -ELSAEAQEESG-RRRSARIAA-------RKKNPMSQSFGKDSHWLHLSP
Cdc27B   286- RKISGRLFSDSGPRR-SSRLSADSGANINSSVATVSGNVNNASKYLGGSK

                                              SEQ ID NO 12
Cdc27A1 321- SESNYAPSLSSMIGKCRIQSSK------EAIPD-TV--------TLNDPA
Cdc27B   335- --------LSSLALRS-VTLRKGHSWANENM-DEGVRGEPFDDSRPNTAS

Cdc27A1 356- TTSGQSVSDTGSSVDDEEKSNPSE--SSPDRFSLIS-GISEVLSILKILG
Cdc27B   375- TTGSMASND----QEDETMSIGGIAMSSQT----ITIGVSEILNLLRTLG

Cdc27A1 403- DGHRHLHMYKCQEALLAYQKLSQKQYNTHWVLMQVGKAYFELQDYFNADS
Cdc27B   417- EGCRLSYMYRCQEALDTYMKLPHKHYNTGWVLSQVGKAYFELIDYLEAEK

Cdc27A1 453- SFTLAHQKYPYALEGMDTYSTVLYHLKEEMRLGYLAQELISVDRLSPESW
Cdc27B   467- AFRLARLASPYCLEGMDIYSTVLYHLKEDMKLSYLAQELISTDRLAPQSW

Cdc27A1 503- CAVGNCYSLRKDHDTALKMFQRAIQLNERFTYAHTLCGHEFAALEEFEDA
Cdc27B   517- CAMGNCYSLQKDHETALKNFLRAVQLNPRFAYAHTLCGHEYTTLEDFENG

Cdc27A1 553- ERCYRKALGIDTRHYNAWYGLGMTYLRQEKFEFAQHQFQLALQINPRSSV
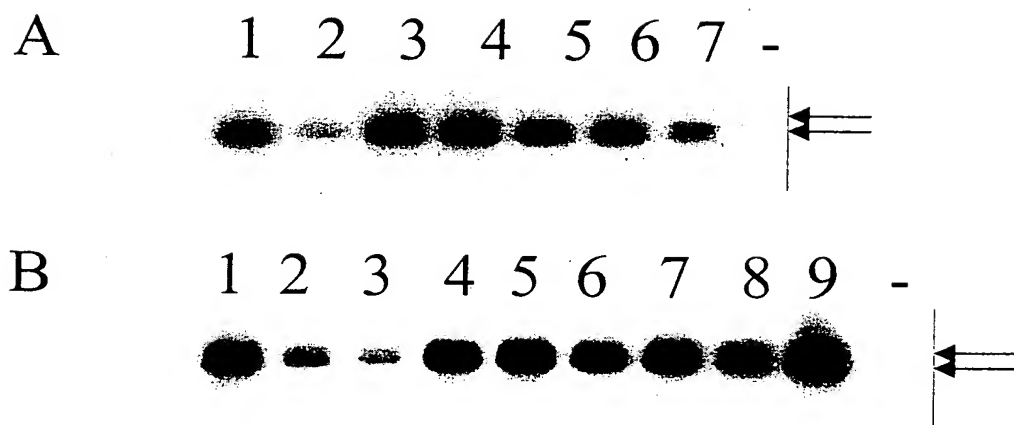Cdc27B   567- MKSYQNALRVDTRHYNAWYGLGMIYLRQEKLEFSEHHFRMAFLINPSSSV

Cdc27A1 603- IMCYYGIALHESKRNDEALMMEKAVLTDAKNPLPKYYKAHILTSLGDYH
Cdc27B   617- IMSYLGTSLHALKRSEEALEIMEQAIVADRKNPLPMYQKANILVCLERLD

Cdc27A1 653- KAQKVLEELKECAPQESSVHASL-GKIYNQLKQYDKAVLHFGIALDLSPS
Cdc27B   667- EALEVLEELKEYAPSESSVYA-LMGRIYKRRNMHDKAMLHFGLALDMKPP

                            SEQ ID NO 7
Cdc27A1 702- PSDAVKIKAYMERLILPDELVTEENL
Cdc27B   716- ATDVAAIKAAMEKLHVPDEIDESP

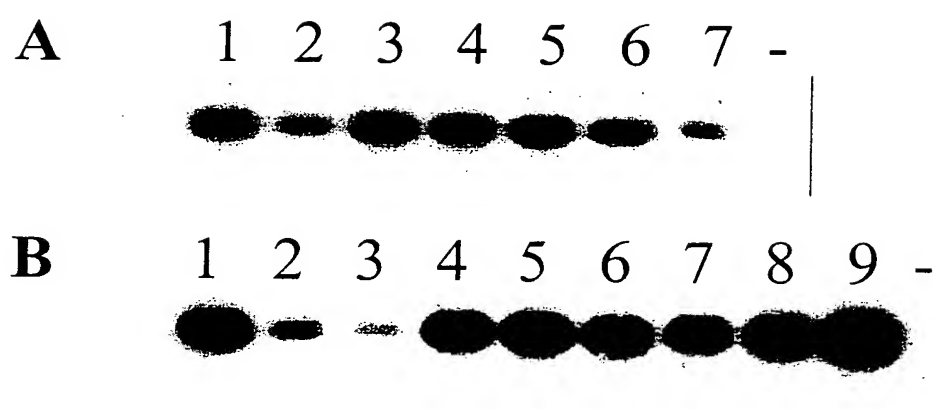# FIGURE 6

FIGURE 7

FIGURE 8